



Title: About wine yeast diversity: adaptation to grape must and its unexpected consequences.

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Abstract content:

Your abstract structure should have an introduction, objective, method, findings, and conclusion. Please add all formatting that you wish to feature in the final abstract book.

Ensure that the text is no longer than 250 words in total.

What drives the diversity of *S. cerevisiae* yeast strains that perform wine fermentation?

Genetic and genomic studies over the past 20 years have shown that wine and flor strains form differentiated populations. Using genomic approaches, we identified and demonstrated the role of the alleles of several genes in the adaptation to the velum of biologically aged wines and confirmed the role of others in the wine environment.

In order to better understand how yeast adapted to the wine environment, we sought to recapitulate wine yeast adaptation using three recombinant populations derived from wine strains, Mediterranean oak strains (as a grape must-naïve population), or crosses between strains from both origins. These populations were grown for 24 consecutive fermentations in a typical Sauvignon grape must. This experimental evolution improved the fitness of the recombinant Mediterranean oak/wine populations and revealed shifts in allelic frequencies at specific regions, including *SSU1* and *ECM34*, which are involved in sulfite resistance; *MET10*, which is involved in sulfide reduction, as well as other regions.

Finally, while studying the characteristic copper adaptation of wine yeast we observed an unexpected consequence: amplification of the *CUP1* genes activates the sulfur assimilation pathway, which may lead to excessive H₂S production.

In conclusion, adaptation of *S. cerevisiae* to the wine environment has been a complex process involving variation across multiple genomic regions, with some adaptive genetic changes impairing wine quality.